

Proteomics Informatics Spring 2024 (BMSC-GA 4437)

Room: Science Building, 435 East 30th St, 9th Floor, Room 909

Zoom: <https://nyu.zoom.us/j/97948183474?pwd=UGdmY29EWm1oU3VPTFZNMDV0cGIKQT09>

Sign up for leading 2 paper discussions:

https://docs.google.com/spreadsheets/d/1IIAwmWKlvEhQMINovDsOVXflsGoA1_INOjkY8JABlg8/edit?usp=sharing

Lecturers:

David Fenyo (David@FenyoLab.org), Professor

Beatrix Ueberheide (Beatrix.Ueberheide@nyumc.org), Associate Professor

Drew Jones (Drew.Jones@nyulangone.org), Assistant Professor

Teaching Assistant:

Will Jogle (William.Jogle@nyulangone.org), PhD Student

Course overview

This course will give an introduction of proteomics and mass spectrometry workflows, experimental design, and data analysis with a focus on algorithms for extracting information from experimental data. The following subjects will be covered in: (1) Protein identification (peptide mass fingerprinting, tandem mass spectrometry, database searching, spectrum library searching, de novo sequencing, significance testing); (2) Protein characterization (protein coverage, top-down proteomics, post-translational modifications, protein processing and degradation, protein complexes); (3) Protein quantitation (metabolic labeling - SILAC, chemical labeling, label-free quantitation, spectrum counting, stoichiometry, biomarker discovery and verification). Examples will be provided throughout the course on how the different approaches can be applied to investigate biological systems. The class will be structured to include hands-on practical techniques for analyzing relevant proteomics datasets.

Learning objectives

At the conclusion of the course, the student will be able to:

Understand experimental design for mass spectrometry based proteomics;

Demonstrate detailed understanding of the possibilities and limitations of algorithms that are applied to proteomics data; and

Analyze a large proteomics data set using available algorithms.

Course Assessment

- Readings and participation (40%): Students are required to attend class, to complete reading assignments and to participate in discussions and engage in healthy exchange of ideas. Each student is required to lead at least one reading from the assigned weekly readings.
- Quizzes (20%): a quiz should be completed before each class
- Final project (40%)

The assignments must be turned in on time and no late assignments will be accepted.

If there is a time that you believe that there is a mistake in grading an assignment/exam, you will have a chance to appeal your exam grade within a week after you receive your grade. If you think this is the case, you must write a note describing the error, attach it to the original exam, and give it to me within a week of the return of your exam. I will review your argument and my initial grading, and then return your exam with a decision to you in a timely manner.

General Policies

Late/missed work: You must adhere to the due dates for all required submissions. If you miss a deadline, then you will not get credit for that assignment/post. Try to avoid last minute submissions.

Incompletes: No "Incompletes" will be assigned for this course unless we are at the very end of the course and you have an emergency.

Responding to Messages: I will check emails daily during the week, and I will respond to course related questions within 48 hours.

Announcements: I will make announcements throughout the semester by email. Make sure that your email address is updated; otherwise you may miss important emails from me.

Safeguards: Always back up your work in a safe place (electronic file with a backup is recommended) and make a hard copy. Do not wait for the last minute to do your work. Allow time for deadlines.

Plagiarism: Plagiarism, the presentation of someone else's words or ideas as your own, is a serious offense and will not be tolerated in this class. The first time you plagiarize someone else's work, you will receive a zero for that assignment. The second time you plagiarize, you will fail the course with a notation of academic dishonesty on your official record.

Schedule

Captions and instructions:

Please attend in person as much as possible.

Hybrid lecture: Read all the background and discussion papers, complete the quiz, and prepare one question for each paper before the lecture.

Pre-recorded lecture: Watch and read any background papers and complete the quiz before next Thursday.

Discussion, presentation or lab: Read all the discussion papers and prepare one question for each paper before the lecture.

1. Lecture: Introduction: Proteomics (January 25, 2024 at 5:30pm, Science Building Room 909)

Lecturer: Fenyo

Slides:

https://docs.google.com/presentation/d/1abP9oIxLutdTILYz9hgActuskBdvsMV7qHMOO_hDqq0

Recording:

https://nyu.zoom.us/rec/share/Lqxgc_5dfDIi5sL_D19jwczMyxgDBUwkN6WcWDqYzw_6F000q6PEXUZSsPyEbPMt.zhr19ZsKnDBA_RuE

Background Readings:

- A. Bensimon, A.J.R. Heck R. Aebersold, "Mass Spectrometry–Based Proteomics and Network Biology", Annual Review of Biochemistry 81 (2012) 379-405, <https://www.annualreviews.org/doi/abs/10.1146/annurev-biochem-072909-100424>.
- Lundberg E, Borner GHH. Spatial proteomics: a powerful discovery tool for cell biology. Nat Rev Mol Cell Biol. 2019, <https://doi.org/10.1038/s41580-018-0094-y>.

Complete Quiz 1 on background readings before class:

<https://forms.gle/UiPDpU1Nxs5YuMtg9>

2. Lecture: Mass spectrometry I, take-home video (64 min)

Recording: https://youtu.be/BUOJILZCwHE?si=FJvxwX-Lrxjx_Uly

Watch before lecture on February 1

3. Lecture: Mass spectrometry II, take-home video (46 min)

Recording: https://www.youtube.com/watch?v=24qMTral_MI&t=1578s

Watch before lecture on February 1

4. Lecture: Interpretation of mass spectra & denovo sequencing I (February 1, 2024 at 5:30pm, Science Building Room 909)

Lecturer: Ueberheide

Slides: https://docs.google.com/presentation/d/1nYGGZgoigNd_Vy103t-n4xmqu7CyBGbq

Cheat Sheet:

<https://docs.google.com/presentation/d/1MOplyBzSTI7YtFJlSM1rLrYT33aGjm/edit?usp=sharing&oid=116679542618952778428&rtpof=true&sd=true>

Background Reading

- Seidler J, Zinn N, Boehm ME, Lehmann WD, "De novo sequencing of peptides by MS/MS, Proteomics 10 (2010) 634-49, <https://doi.org/10.1002/pmic.200900459>.

- Addona T, Clauser K: De novo peptide sequencing via manual interpretation of MS/MS spectra, Curr Protoc Protein Sci. 2002, <https://doi.org/10.1002/0471140864.ps1611s27>.

Before this class, complete Quiz 2 on background readings and lectures on mass spectrometry: <https://forms.gle/KfsGFHFZTDUEXhj4A>

5. Lecture: Interpretation of mass spectra & denovo sequencing II (take-home video (45 min), watch **before lecture on February 8**)

Recordings:

Part 1: https://youtu.be/rm1YwieTOqY?si=m4E6KY_8Nz3qIKIS

Part 2: https://youtu.be/_vJutitnFVI?si=5tbOWhmJgFZRzucr

6. Lab: Interpretation of mass spectra & denovo sequencing III (February 8, 2023 at 5:30pm, Science Building Room 909)

Lecturer: Ueberheide

Slides: https://docs.google.com/presentation/d/11BKRWiVx8LqtpjkwvWgl7AE_leQBL4MT

Spectra: https://docs.google.com/presentation/d/1H_ZBIkLYjP6SkLkPkEIIxFaxFSsHQI02

Recording:

Before this class, complete Quiz 3: <https://forms.gle/DQQavGhEYpUF6ej1A>

7. Lecture: Signal Processing (take-home video (70 min), watch **before lecture on February 15**)

Slides:

http://fenyolab.org/presentations/Proteomics_Informatics_2015/slides/Proteomics-Informatics-WEEK-3.pptx

Recording: http://youtu.be/_bhuki3x-5o

8. Lecture: Protein identification (take-home video (114 min), watch **before lecture on February 15**)

Slides:

<https://docs.google.com/presentation/d/1ER4U-W5isvhRWlwlXseB7UugU3hly2XCgBkagdUwc4k/edit?usp=sharing>

Recording:

<https://nyu.zoom.us/rec/share/TiMJqVOBhqoMoSBsSQeWLNFOjWgP-m7p4kaURHdZcrFYAP3GhghQtSueqEK4tQJS.vF0JsF1wGmgy-e1K>

Background Reading:

- D. Fenyő, J. Eriksson, R. Beavis, "Mass spectrometric protein identification using the global proteome machine", Methods Mol Biol 673 (2010) 189-202.

9. Discussion: Protein identification (February 15, 2024 at 5:30pm, Science Building Room 909)

Slides:

https://docs.google.com/presentation/d/1xumlxrPYC4Q2fp_wYDPsOP8CDZoXeVoPIfAtG1TaGW0

Recording:

https://nyu.zoom.us/rec/share/Z3-OsELip5n3iLzGGeLNyOS1uW4XHDt4OVOJbX_AhppOekd1JrF87AnJ7TcVVYA_.HIHjX0pIGNCUyE01

Discussion papers:

- Pavel Sinitcyn, Jan Daniel Rudolph, Jürgen Cox: Computational Methods for Understanding Mass Spectrometry–Based Shotgun Proteomics Data, Annual Review of Biomedical Data Science 2018 1:1, 207-234, <https://www.annualreviews.org/doi/abs/10.1146/annurev-biodatasci-080917-013516>.
- Elias, J.E. & Gygi, S.P.: "Target-decoy search strategy for increased confidence in large-scale protein identifications by mass spectrometry" Nat. Methods 4, 207-214 (2007), <https://doi.org/10.1038/nmeth1019>.
- C. Warinner, K. Korzow Richter, and M.J. Collins: Paleoproteomics, Chemical Reviews 122, (2022) 13401-13446, <https://doi.org/10.1021/acs.chemrev.1c00703>.
- Gessulat, S., Schmidt, T., Zolg, D.P. et al. Prosit: proteome-wide prediction of peptide tandem mass spectra by deep learning, Nat Methods 16, 509–518 (2019), <https://doi.org/10.1038/s41592-019-0426-7>.

Before the discussion: prepare one question for each discussion paper and the lectures on signal processing and mass spectrometry, and complete Quiz 4:

<https://forms.gle/GVCH5JMYrNAwHHKX7>.

10. Lecture: Protein quantitation Overview (take-home video (114 min), watch **before discussion on February 22**)

Slides:

https://docs.google.com/presentation/d/1tN5ZQt36K8je_NSmILSvpeLTJdHjygluNXen-xRo5qc/e/dit?usp=sharing

Recording:

https://nyu.zoom.us/rec/share/F0Vuy3in0kgrqoltZGB6YbsJ0Jm3VayUIVPR_jw3hJT7MQBi1Z3z0CGSPFtuzqp.rq8T2y-BH_nwp27Z

Background Reading:

- M.A. Gillette, S.A. Carr, "Quantitative analysis of peptides and proteins in biomedicine by targeted mass spectrometry", Nature Methods 10 (2013) 28–34.
- D.R. Mani, S.E. Abbatiello, S.A. Carr, "Statistical characterization of multiple-reaction monitoring mass spectrometry (MRM-MS) assays for quantitative proteomics", BMC Bioinformatics 13 (2012) S9.

11. Lecture: Protein quantitation (take-home video (61 min), watch **before discussion on February 22**)

Recording: <https://youtu.be/AQchAPIfkGA?si=Ckc7WmZVQ3Hz9LDr>

12. Lecture: Protein quantitation: multiple reaction monitoring (take-home video (41 min), watch **before discussion on February 22**)

Slides:

http://fenyolab.org/presentations/Proteomics_Informatics_2015/slides/Proteomics-Informatics-Week-7.pptx

Recording: <http://youtu.be/9ltCwDRMovg>

13. Lecture: Protein quantitation (take-home video (56 min), watch **before discussion on February 22**)

Recording:

https://nyu.zoom.us/rec/share/-zLpoEjS5K54gybe-xwki3e4-1z-qEmlDK_CyGO_Gtc6HUCVVOSbTiJllzsKA4O9.ylf7o6V7_mcNHICL

Background Reading:

- Tyanova, S., Temu, T., and Cox, J., The MaxQuant computational platform for mass spectrometry-based shotgun proteomics, *Nat Protocols*, 2016, 11, pp 2301–2319
- Pino LK et al., The Skyline ecosystem: Informatics for quantitative mass spectrometry proteomics. *Mass Spectrom Rev.* 2017

14. Discussion: Protein quantitation (February 22, 2024)

Slides:

https://docs.google.com/presentation/d/12bK4c0Uh1upB22TE16mQbktKze_qeE4YYst2J1S8O0Y

Recording:

https://nyu.zoom.us/rec/share/oZWICGzYcSrQlaaYmVylwUtMIeqRVFURAhq9liflcBIJ_kZXa7Yh4UwFZVJ-0bcL.xMHQb1qCLjSxrl-o

Discussion papers:

- Domon & Aebersold: Options and considerations when selecting a quantitative proteomics strategy, *Nat. Biotechnol* 28, 710-721 (2010), <https://doi.org/10.1038/nbt.1661>.
- van Bentum & Selbach: An Introduction to Advanced Targeted Acquisition Methods, *Molecular & Cellular Proteomics*, Vol. 20100165, 2021, [https://www.mcponline.org/article/S1535-9476\(21\)00137-7/fulltext](https://www.mcponline.org/article/S1535-9476(21)00137-7/fulltext).
- Gillet et al.: Targeted data extraction of the MS/MS spectra generated by data-independent acquisition: a new concept for consistent and accurate proteome analysis, *Mol Cell Proteomics* 11 (2012) O111.016717. <https://doi.org/10.1074/mcp.O111.016717>.
- Shenoy et al.: Proteomic patterns associated with response to breast cancer neoadjuvant treatment, *Molecular Systems Biology* (2020)16:e9443, <https://doi.org/10.15252/msb.20209443>.

Before the discussion: prepare one question for each discussion paper and the lectures on protein quantitation, and complete Quiz 5: <https://forms.gle/cH9UkotyRb2PnEZV6>.

15. Lecture: Protein characterization: post-translational modifications I (take-home video (108 min), watch **before discussion on February 29**)

Recording:

https://nyu.zoom.us/rec/share/8D3ycwxiF_pXG9MhH408YqR9OnMlvPMwsXN3B1un8GCIUfU5CrJO9Wr5dBYVaFXQ.XisjjhuZxsLksK5N

16. Lecture: Protein characterization: post-translational modifications II (take-home video (50 min), watch **before discussion on February 29**)

Recording: <http://youtu.be/mJTJ-8iW9Co>

17. Discussion: Protein characterization: post-translational modifications (February 29, 2024)

We are using a different Zoom link for this class:

<https://nyulangone.zoom.us/j/96556439448?pwd=ODJGQnJyT3V1dTdhN05LOFVsLzBhZz09> (Meeting ID: 965 5643 9448, Passcode: 888376)

Discussion papers:

- Leutert et al.: Decoding Post-Translational Modification Crosstalk With Proteomics, Molecular & Cellular Proteomics, Volume 20, 100129, <https://doi.org/10.1016/j.mcpro.2021.100129>.
- Lu et al.: Accelerating the Field of Epigenetic Histone Modification Through Mass Spectrometry–Based Approaches, Molecular & Cellular Proteomics, Volume 20, 100006, <https://doi.org/10.1074/mcp.r120.002257>.
- Delafield & Li: Recent Advances in Analytical Approaches for Glycan and Glycopeptide Quantitation, Molecular & Cellular Proteomics, Vol. 20100054, 2021, [https://www.mcponline.org/article/S1535-9476\(21\)00027-X/fulltext](https://www.mcponline.org/article/S1535-9476(21)00027-X/fulltext).
- Geffen et al.: Pan-cancer analysis of post-translational modifications reveals shared patterns of protein regulation, Cell 186 (2023) 3945-3967.e26, <https://doi.org/10.1016/j.cell.2023.07.013>.

Before the discussion: prepare one question for each discussion paper and the lectures on post-translational modifications, and complete Quiz 6: <https://forms.gle/gkhaYVKnfVp5B7Di7>.

18. Lecture: Introduction to Proteomic Statistical Analysis (take-home video (164 min), watch **before discussion on March 7**)

Recording: <https://www.youtube.com/watch?v=30a6sDj8Qlo>

19. Lab: Protein Identification, Quantitation and Statistical Analysis (March 7, 2024)

20. Discussion: Project Plan Presentations (March 14, 2024 at 5:30pm)

Before the discussion: Select a project and prepare slides for a 7-min presentation that should include background, why you are interested in the project, description of the data, and a preliminary analysis plan.

Spring Break March 18-24, 2024

21. Lecture: Protein characterization: protein interactions I (take-home video (109 min), watch before discussion on March 28)

Recording:

https://nyu.zoom.us/rec/share/FUYdZp94FiPt_kdXHoF6sQAzcW4DR0LjlqLwPy2fW2tjQ2m7LR_S8nPocuGNrHvuB.JfsinhWPsbiruXB7

Background Reading:

- Z Hakhverdyan, M Domanski, LE Hough, AA Oroskar, AR Oroskar, S Keegan, DJ Dilworth, KR Molloy, V Sherman, JD Aitchison, D Fenyö, BT Chait, TH Jensen, MP Rout, J LaCava, "Rapid, optimized interactomic screening", Nature Methods 2015
- A Leitner, R Reischl, T Walzthoeni, F Herzog, S Bohn, F Förster, and R Aebersold, "Expanding the Chemical Cross-Linking Toolbox by the Use of Multiple Proteases and Enrichment by Size Exclusion Chromatography", Mol Cell Proteomics 11 (2012)

22. Lecture: Protein characterization: protein interactions II (take-home video (64 min), watch before discussion on March 28)

Recording: https://youtu.be/_bpt-403xO8?si=NmFCuuW2ix-3hxrz

23. Discussion: Protein characterization: protein interactions (March 28, 2024 at 5:30pm)

Discussion papers:

- Sinz: Cross-Linking/Mass Spectrometry for Studying Protein Structures and Protein-Protein Interactions: Where Are We Now and Where Should We Go from Here? 57 (2018) 6390-6396, <https://doi.org/10.1002/anie.201709559>.
- Salas, Daniela et al.: Next-generation Interactomics: Considerations for the Use of Co-elution to Measure Protein Interaction Networks, Molecular & Cellular Proteomics, 19 (2020) 1 - 10, <https://doi.org/10.1074/mcp.r119.001803>.

- Huttlin et al.: BioPlex 3.0: Dual Proteome-scale Networks Reveal Cell-specific Remodeling of the Human Interactome, Cell 184 (2021) 3022-3040.e28, <https://doi.org/10.1016/j.cell.2021.04.011>.
- Zhu et al.: Evaluation of AlphaFold-Multimer prediction on multi-chain protein complexes, Bioinformatics, 39 (2023) btad424, <https://doi.org/10.1093/bioinformatics/btad424>.

Before the discussion: prepare one question for each discussion paper and the lectures on protein interactions, and complete Quiz 7: <https://forms.gle/cEdqqEsPpcaDTySG6>.

24. Lecture: Metabolomics (take-home video (120 min), watch **before discussion on April 4**)

Recording:

https://nyu.zoom.us/rec/share/QmCnVut3Q8sIF2sDehaN3yHleiiXmeTQRWJBXIo4mpq0757yJp_0qbdbBrLjAoST.sdCaQpCvz1LFYfSY

Background Reading:

- Misra: New software tools, databases, and resources in metabolomics: updates from 2020, Metabolomics 17 (2021) 49, <https://doi.org/10.1007/s11306-021-01796-1>.
- Alseekh et al.: Mass spectrometry-based metabolomics: a guide for annotation, quantification and best reporting practices. Nat Methods 18 (2021) 747-756, <https://doi.org/10.1038/s41592-021-01197-1>.

25. Discussion: Metabolomics (April 4, 2024 at 5:30pm)

Lecturer: Jones

Slides: <https://docs.google.com/presentation/d/1MdXQVPBb-WPorogdRBk6qoBBWEgn2rmK>

Recording:

https://nyu.zoom.us/rec/share/Fiuf3qVKMVLINPTFNMusKYw_dezAAkIntC7Z8V4u9Kafd7ouwv045ppO7YvD21Y.ehUDJXMf1gDogXh

Discussion papers:

- Li et al.: Spectral entropy outperforms MS/MS dot product similarity for small-molecule compound identification. Nat Methods. 2021 Dec;18(12):1524-1531. <https://doi.org/10.1038/s41592-021-01331-z>.
- Schmid et al.: Ion identity molecular networking for mass spectrometry-based metabolomics in the GNPS environment. Nat Commun. 2021 Jun 22;12(1):3832. <https://doi.org/10.1038/s41467-021-23953-9>.
- Borelli et al.: Improving annotation propagation on molecular networks through random walks: introducing ChemWalker, Bioinformatics 39(2023) btad078, <https://doi.org/10.1093/bioinformatics/btad078>.
- Zuffa et al.: A Taxonomically-informed Mass Spectrometry Search Tool for Microbial Metabolomics Data, Res Sq [Preprint] 2023 rs.3.rs-3189768, <https://doi.org/10.21203/rs.3.rs-3189768/v1>.

Before the discussion: prepare one question for each discussion paper and the lectures on post-translational modifications, and complete Quiz 8:

<https://forms.gle/qFSqaKigfZs45X8bA>.

26. Lecture: Proteogenomics (April 11, 2024 at 5:30pm)

Lecturer: Fenyö

Slides:

https://docs.google.com/presentation/d/1-5m73w2CldMWMMUOlcLcbL_pXPNSC1TAgc-BqSA1PaE

Recording:

https://nyu.zoom.us/rec/share/7wgqWpG4I8aiREAwafjFN626uuqVJBVwMd2UrbPol4ajGpXW-ubqsl6Rvnpmo-.GwBO_INMpWeWMXHI

Before the lecture: prepare one question for each background paper.

Background Reading:

- Ruggles KV, Krug K, Wang X, Clauser KR, Wang J, Payne SH, Fenyö D, Zhang B, Mani DR. Methods, Tools and Current Perspectives in Proteogenomics. Mol Cell Proteomics 2017, <https://doi.org/10.1074/mcp.mr117.000024>.

27. Lecture: Protein characterization: MHC Peptides (take-home video (85 min), watch **before discussion on April 18**)

Recording:

https://nyu.zoom.us/rec/share/95wbEXEsQoPMN65zxqTzqjzaVBJ4E0P09gz_HKVJ6YzBnZzqZaS8ET3lmuLlwNjl.eX6M6OvVrn8qUZ0Q

Background Reading:

- Purcell AW, Ramarathinam SH, Ternette N. Mass spectrometry-based identification of MHC-bound peptides for immunopeptidomics. Nat Protoc. 2019 Jun;14(6):1687-1707.
- Freudenmann LK, Marcu A, Stevanovic S. Mapping the tumour human leukocyte antigen (HLA) ligandome by mass spectrometry. Immunology. 2018 Jul;154(3):331-345.

28. Lecture: Top Down Proteomics (take-home video, watch **before discussion on April 18**)

Recording: <https://youtu.be/d42ZsbE5nL4?si=EFIVnTGBZw83riG3>

29. Lecture: Single-Cell Proteomics (take-home video, watch **before discussion on April 18**)

Recording: <https://youtu.be/1t0jugs2lcs?si=oXNZNOMdkQM435Sg>

Background Reading:

- Slavov. Scaling Up Single-Cell Proteomics 21 (2021) 100179. <https://doi.org/10.1016/j.mcpro.2021.100179>

30. Discussion: Proteogenomics, MHC Peptides, Top Down, Single-Cell, and Plasma Proteomics (April 18, 2024 at 5:30pm)

Discussion papers:

- Dou, Katsnelson & Gritsenko et al.: Proteogenomic insights suggest druggable pathways in endometrial carcinoma, Cancer Cell 41 (2023) 1586-1605.e15. <http://doi.org/10.1016/j.ccell.2023.07.007>.

- Qi et al.: Proteogenomic Analysis Unveils the HLA Class I-Presented Immunopeptidome in Melanoma and EGFR-Mutant Lung Adenocarcinoma, Mol Cell Proteomics 20 (2021) 100136, <https://doi.org/10.1016/j.mcpro.2021.100136>.
- Lloyd M. Smith et al.: The Human Proteoform Project: Defining the human proteome, Sci. Adv. 7 (2021) eabk0734, <https://doi.org/10.1126/sciadv.abk0734>.
- Huffman et al.: Prioritized mass spectrometry increases the depth, sensitivity and data completeness of single-cell proteomics, Nat Methods. 20 (2023) 714-722, <https://doi.org/10.1038/s41592-023-01830-1>.
- Eldjarn et al.: Large-scale plasma proteomics comparisons through genetics and disease associations. Nature 622, 348–358 (2023), <https://doi.org/10.1038/s41586-023-06563-x>.

Before the discussion: prepare one question for each discussion paper and the lectures on post-translational modifications, and complete Quiz 9:
<https://forms.gle/NMG3QLRK94QNfVVFA>.

31. Lecture: Spatial Proteomics (take-home video, watch **before discussion on April 25**)

Recording:

https://nyu.zoom.us/rec/share/2G9ZhdLYXHK24etug1VZPcn7tdxUGU6njtj6-mtKjm2pHssOAntcEn3oXVQ_O3Fu.r-ih56lu6WCBSvkO

Background Reading:

- Schürch et al.: Coordinated Cellular Neighborhoods Orchestrate Antitumoral Immunity at the Colorectal Cancer Invasive Front. Cell. 2020 Oct 29;183(3):838. doi: 10.1016/j.cell.2020.10.021. Erratum for: Cell. 2020 Sep 3;182(5):1341-1359.e19.

32. Lecture: Spatial Proteomics (April 25, 2024 at 5:30pm)

Slides:

<https://docs.google.com/presentation/d/1Ishxydl7rQsCK2XWS5We06-3xrG15YwyWJWR0SyDKJl>

Recording:

https://nyu.zoom.us/rec/share/YFAEM1rp-DDJXuQ55o4gXh2xVYTo57fqL4JWnhmscqT57t0ggsqZ-44n25AiywF_.X6YBBOny1Xe9BePf

33. Lecture: Spatial Mass Spectrometry (May 2, 2024 at 5:30pm)

Lecturer: Jones

Recording:

https://nyu.zoom.us/rec/share/d6L-98ZdxbwB2gzYJdaAuGE6dZy4FF3HgMnJKjUIb5im5xakKo-GTZNDhf-1r7ZQ.FNkSnQ24Y8N_YiRM

Background Reading:

- Theodore Alexandrov: Spatial Metabolomics and Imaging Mass Spectrometry in the Age of Artificial Intelligence, Annu Rev Biomed Data Sci. 2020 Jul; 3: 61–87. <https://doi.org/10.1146%2Fannurev-biodatasci-011420-031537>.

34. Discussion: Project Presentations (Friday May 10, 2024 at 4pm)

Please fill out two course evaluations:

1. <https://forms.gle/5w2fcou5chY5WMga9>

2. https://nyumc.qualtrics.com/jfe/form/SV_egPNxKWPCM8wsHc